

The peptides PAFSPAFDQL(pY)(pY)WDQNSSEQG ("b-N1219Q") (SEQ ID NO:72) and PAFSPAFDL(pY)(pY)WDQNSSEQG ("b-N1219D") (SEQ ID NO:73) which carried point mutations in the asparagine residue in the ninth position, also show substantially reduced binding to the PTB domain in these assays (Figure 3).

IN THE CLAIMS

Please amend the following claims:

1. (Amended) A substantially pure peptide which is capable of binding a PTB domain, wherein the peptide is from 5 to 100 amino acids in length, and comprises a core sequence of aminoacids $NX_3X_1X_2X_4$;

wherein X_1 is selected from the group consisting of Y, pY or an analog thereof, E, T, D, Q, A and F;

X_2 is selected from pY or an analog thereof, and Y, provided that at least one of X_1 and X_2 is pY, or an analog thereof;

X_3 is selected from the group consisting of L and A; and

X_4 is selected from the group consisting of W, L, S, F and Q (SEQ ID No:1).

2. (Amended) The peptide as recited in claim 1, wherein the peptide is from 6 to 100 amino acids in length, and comprises a core sequence of amino acids $X_5NX_3X_1X_2X_4$, wherein X_5 is selected from the group consisting of D, S, E and A (SEQ ID NO:2).

4. (Amended) The peptide as recited in claim 3, wherein the peptide is from 6 to 100 amino acids in length, and comprises a core sequence of amino acids selected from the group consisting of $DNX_3X_1pYX_4$ (SEQ ID NO:3) and $ENX_3X_1pYX_4$ (SEQ ID NO:4), where X_4 is selected from the group consisting of W and F.

5. (Amended) The peptide as recited in claim 2, wherein the peptide is from 12 to 100 amino acids in length, and comprises a core sequence of amino acids selected from the

group consisting of AFDNLY(pY)WDQNS (SEQ ID NO:5), AFDNL(PY)YWDQNS (SEQ ID NO:6) and AFDNL(pY)(pY)WDQNS (SEQ ID NO:7).

6. (Amended) The peptide as recited in claim 2, wherein the peptide is from 21 to 100 amino acids in length, and comprises a core sequence of amino acids selected from the group consisting of: PAFSPAFDNLY(pY)WDQNSSEQG (SEQ ID NO:8); PAFSPAFDNL(pY)YWDQNSSEQG (SEQ ID NO:9); PAFSPAFDNL(pY)(pY)WDQNSSEQG (SEQ ID NO:10); PAFSPAADNLY(pY)WDQNSSEQG (SEQ ID NO:11); PAFSPAADNL(pY)YWDQNSSEQG (SEQ ID NO:12); PAFSPAADNL(pY)(pY)WDQNSSEQG (SEQ ID NO:13); PAFSPAFANLY(pY)WDQNSSEQG (SEQ ID NO:14); PAFSPAFANL(pY)YWDQNSSEQG (SEQ ID NO:15); PAFSPAFANL(pY)(pY)WDQNSSEQG (SEQ ID NO:16); PAFSPAFSNLY(pY)WDQNSSEQG (SEQ ID NO:17); PAFSPAFSNL(pY)YWDQNSSEQG (SEQ ID NO:18); PAFSPAFSNL(pY)(pY)WDQNSSEQG (SEQ ID NO:19); PAFSPAFDNAY(pY)WDQNSSEQG (SEQ ID NO:20); PAFSPAFDNA(pY)YWDQNSSEQG (SEQ ID NO:21); PAFSPAFDNA(pY)(pY)WDQNSSEQG (SEQ ID NO:22); PAFSPAFDNLA(pY)WDQNSSEQG (SEQ ID NO:23); PAFSPAFDNLF(pY)WDQNSSEQG (SEQ ID NO:24); PAFSPAFDNLY(pY)FDQNSSEQG (SEQ ID NO:25); PAFSPAFDNL(pY)YFDQNSSEQG (SEQ ID NO:26); PAFSPAFDNL(pY)(pY)FDQNSSEQG (SEQ ID NO:27); PAFSPAFDNLY(pY)WAQNSSEQG (SEQ ID NO:28); PAFSPAFDNL(pY)YWAQNSSEQG (SEQ ID NO:29); PAFSPAFDNL(pY)(pY)WAQNSSEQG (SEQ ID NO:30); PAFSPAFDNLY(pY)WDANSSEQG (SEQ ID NO:31); PAFSPAFDNL(pY)YWDANSSEQG (SEQ ID NO:32); PAFSPAFDNL(pY)(pY)WDANSSEQG (SEQ ID NO:33); PAFSPAFDNLY(pY)WDNNSSEQG (SEQ ID NO:34); PAFSPAFDNL(pY)YWDNNSSEQG (SEQ ID NO:35); PAFSPAFDNL(pY)(pY)WDNNSSEQG (SEQ ID NO:36); PAFSPAFDNLY(pY)WDDNSSEQG (SEQ ID NO:37); PAFSPAFDNL(pY)YWDDNSSEQG (SEQ ID NO:38); PAFSPAFDNL(pY)(pY)WDDNSSEQG (SEQ ID NO:39); PAFSPAFDNLY(pY)WDQASSEQG (SEQ ID NO:40); PAFSPAFDNL(PY)YWDQASSEQG

(SEQ ID NO:41); PAFSPAFDNL(pY)(pY)WDQASSEQG (SEQ ID NO:42);
PAFSPAFDNLY(pY)WDQNASEQG (SEQ ID NO:43);
PAFSPAFDNL(pY)YWDQNASEQG (SEQ ID NO:44); and
PAFSPAFDNL(pY)(pY)WDQNASEQG (SEQ ID NO:45).

8. (Amended) A substantially pure peptide which is capable of binding a PTB domain, wherein the peptide is from 21 to about 100 amino acids in length and which comprises a core sequence of amino acids selected from the group consisting of AFGGAVENPE(pY)LAPRAGTASQ (SEQ ID NO:46) and EGTPTAENPE(pY)LGLDVPV (SEQ ID NO:47).

10. (Amended) A method of determining whether a protein comprises a PTB domain, comprising the steps of:

contacting the protein with a peptide, which peptide is from 5 to 100 amino acids in length and comprises a core sequence of amino acids $NX_3X_1X_2X_4$, wherein X_1 is selected from the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is selected from the group consisting of L and A; and X_4 is selected from the group consisting of W, L, S, F and Q (SEQ ID NO:1); and determining whether the peptide binds to the protein during said contacting step, where the binding of the peptide to the protein is indicative that the protein comprises a PTB domain.

13. (Amended) A method of determining whether a test compound is an agonist or antagonist of a PTB/phosphorylated ligand interaction, comprising the steps of:

incubating the test compound with a protein comprising a PTB domain and a peptide, which peptide is from 5 to 100 amino acids in length and which comprises a core amino acid sequence $NX_3X_1X_2X_4$, wherein X_1 is selected from the group consisting of Y, pY, E, T, D, Q, A and F; X_2 is selected from pY and Y, provided that at least one of X_1 and X_2 is pY; X_3 is selected from the group consisting of L and A; and X_4 is selected from the group consisting of W, L, S, F and Q (SEQ ID NO:1); and